Amendments to the Claims:

The listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-13 (canceled)

Claim 14 (currently amended): A method of identifying an agent that modulates expression of at least one gene in a granulocyte cell population in a patient with a sterile inflammatory disease in a patient, comprising,

(a) isolating a granulocyte population from a patient with a sterile inflammatory disease;

(b) treating the granulocyte population with an agent;

(c) preparing a gene expression profile of said granulocyte population;

(d) comparing the gene expression profile of step (c) to at least one gene expression profile of an untreated granulocyte population from the subject patient known to have a sterile inflammatory disease, to identify agents that modulate expression of at least one gene in a granulocyte cell population associated with a sterile inflammatory disease.

Claim 15 (previously presented): The method of claim 14, wherein the sterile inflammatory disease is selected from the group consisting of glomerulonephritis, psoriasis, rheumatoid arthritis, asthma, cardiac and renal reperfusion injury, thrombosis, adult respiratory distress syndrome, periodontal disease and inflammatory bowel disease.

Claim 16 (previously presented): The method of claim 15, wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

Claim 17 (previously presented): The method of claim 14, wherein the sterile inflammatory disease is glomerulonephritis.

Claim 18 (previously presented): The method of claim 14, wherein the granulocyte population is a neutrophil population, an eosinophil population, a basophil population, or a combined population of different granulocytic cells.

Claim 19 (currently amended): A method of identifying an agent that modulates expression of at least one gene in a granulocyte cell population in a patient with a sterile inflammatory disease in a patient comprising,

(a) treating polymorphonuclear white blood cells from a patient known to have sterile inflammatory disease with an agent;

(b) preparing a gene expression profile from said polymorphonuclear white blood cells; and

(c) comparing the gene expression profile of step (b) to at least one gene expression profile of untreated polymorphonuclear white blood cells from the subject patient known to have a sterile inflammatory disease, to identify agents that modulate expression of at least one gene in a granulocyte cell population associated with a sterile inflammatory disease.

Claim 20 (currently amended): The method of claim 19, wherein the sterile inflammatory disease is selected from the group consisting of glomerulonephritis, psoriasis, rheumatoid rheumatorid arthritis, asthma, cardiac and renal reperfusion injury, thrombosis, adult respiratory distress syndrome, periodontal disease and inflammatory bowel disease.

Claim 21 (previously presented): The method of claim 19, wherein the inflammatory bowel disease is Crohn's disease or ulcerative colitis.

Claim 22 (previously presented): The method of claim 19, wherein the sterile inflammatory disease is glomerulonephritis.

Claim 23 (previously presented): The method of claim 19, wherein the polymorphonuclear white blood cells are neutrophils, eosinophils, basophils, or a combination of different polymorphonuclear white blood cells.

Claim 24 (previously presented): The method of claim 19, wherein the polymorphonuclear white blood cells are neutrophils.

Claim 25 (currently amended): A method of identifying an agent that modulates expression of at least one gene in a granulocyte cell population in a patient with a sterile inflammatory disease comprising glomerulonephritis in a patient, comprising the steps of:

(a) isolating polymorphonuclear white blood cells from a patient with a glomerulonephritis;

(b) treating the polymorphonuclear white blood cells with an agent;

(c) isolating RNA from the isolated polymorphonuclear white blood cells;

(d) preparing a gene expression profile from the isolated RNA; and

(e) comparing the gene expression profile of step (d) to at least one gene expression profile of untreated polymorphonuclear white blood cells from the subject patient known to have glomerulonephritis to identify agents that modulate expression of at least one gene in a granulocyte cell population associated with glomerulonephritis.

Claim 26 (previously presented): The method of claim 25, wherein the polymorphonuclear white blood cells are neutrophils, eosinophils, basophils, or a combination of different polymorphonuclear white blood cells.

Claim 27 (previously presented): The method of claim 25, wherein the polymorphonuclear white blood cells are neutrophils.

Claim 28 (previously presented): The method of claim 14, wherein the granulocyte population is from peripheral blood.

Claim 29 (previously presented): The method of claim 19, wherein the polymorphonuclear white blood cells are isolated from peripheral blood.

Claim 30 (previously presented): The method of claim 25, wherein the polymorphonuclear white blood cells are isolated from peripheral blood of the patient.

Claim 31 (previously presented): A method of any one of claims 14, 19 or 25. wherein the expression profile comprises the expression level of at least about 5 genes.

Claim 32 (previously presented): The method of any one of claims 14, 19 or 25, wherein the expression profile comprises the expression level of at least about 10 genes.

Claim 33 (previously presented): The method of any one of claims 14, 19 or 25, wherein the expression profile comprises the expression level of at least about 50 genes.

Claim 34 (currently amended): The method of ~~claims~~ any one of claims 14, 19 or 25, wherein the expression profile comprises the expression level of at least about 100 genes.

Claim 35 (currently amended): The method of ~~claims~~ any one of claims 14, 19 or 25, wherein the expression profile is prepared by hybridization of nucleic acids to nucleic acids immobilized on a solid substrate.

Claim 36 (previously presented): The method of claim 35, wherein the solid substrate is selected from the group consisting of nitrocellulose membrane, nylon membrane, silicon wafer, and borosilicate slide.

Claim 37 (new): The method of any one of claims 14, 19, or 25, wherein at least one of the gene expression profiles is digitized.